AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-19. (cancelled).

20. (currently amended) A ~~synthetic DNA promoter, said~~ promoter comprising at least one of each of the following elements (i)-(ix), or functional fragments thereof, in the 5' to 3' direction:

(i) domain II which comprises at least one member selected from the group consisting of subdomain II (a), subdomain II (b), subdomain II (c), subdomain II (d) and domain III, wherein subdomain II (a) is SEQ ID NO: 7, or subdomain II (a) is a functional sequence with at least 50% sequence identity to SEQ ID NO: 7 and activates transcription; ~~subdomain II (b) is SEQ ID NO: 8, or subdomain II (b) is a functional sequence with at least 65% sequence identity to SEQ ID NO: 8; subdomain II (c) is SEQ ID NO: 9, or subdomain II (c) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 9; subdomain II (d) is SEQ ID NO: 10, or subdomain II (d) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 10; and domain III is SEQ ID NO: 11, or domain III is a functional sequence with at least 75% sequence identity to SEQ ID NO: 11~~;

(ii) domain I, which comprises at least one member selected from the group consisting of subdomain I (a), subdomain I (b), and subdomain I (c), wherein subdomain I (a) is SEQ ID NO: 18, or subdomain I (a) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 18 and activates transcription; ~~subdomain I (b) is SEQ ID NO: 19, or subdomain I (b) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 19; and subdomain I (c) is SEQ ID NO: 20, or subdomain I (c) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 20~~;

(iii) minimal domain (b), wherein minimal domain (b) is SEQ ID NO: 5, or minimal domain (b) is a functional sequence with at least 75% sequence identity to SEQ ID NO: 5 and activates transcription;

(iv) minimal domain (a), wherein minimal domain (a) is SEQ ID NO: 2, or minimal domain (a) is a functional sequence at least 75% homologous to SEQ ID NO: 2 and activates transcription~~, or minimal domain (a) is SEQ ID NO: 3, or minimal domain (a) is a functional sequence at least 60% homologous to SEQ ID NO: 3~~;

(v) region between minimal promoter (a) and a transcription start site~~ context~~, wherein said region between minimal promoter (a) and said transcription start site ~~context~~ is SEQ ID NO: 12, or said region between minimal promoter (a) and the transcription start site is a sequence with at least 75% sequence identity to SEQ ID NO: 12;

(vi) transcription start site~~ context~~, wherein said transcription start site ~~context~~ is SEQ ID NO: 4, or said transcription start site ~~context~~ is a functional sequence with at least 50% sequence identity to SEQ ID NO: 4 and activates transcription;

(vii) 5' untranslated leader region, wherein said 5' untranslated leader region is SEQ ID NO: 13, or said 5' untranslated leader region is a sequence with at least 75% sequence identity to SEQ ID NO: 13;

(viii) translational initiation codon~~ context~~, wherein said translational initiation codon ~~context~~ is SEQ ID NO: 14, or said translational initiation codon ~~context~~ is a sequence with at least 75% sequence identity to SEQ ID NO: 14~~, or said translational initiation codon context is SEQ ID NO: 15, or said translational initiation codon context is a sequence with at least 50% sequence identity to SEQ ID NO: 15~~; and

(ix) a polynucleotide encoding the amino acid sequence set forth in ~~codons that encode four N-terminal amino acids in frame with a nucleic acid sequence of a gene to which said promoter is linked, wherein said N-terminal amino acids correspond to~~ SEQ ID NO. 16.

21. (currently amended) The ~~synthetic DNA~~ promoter of claim 20, wherein subdomain II (a) is SEQ ID NO: 7.

22 - 25. (cancelled).

26. (currently amended) The ~~synthetic DNA~~ promoter of claim 20, wherein domain I (a) is SEQ ID NO: 18.

27. (cancelled).

28. (cancelled).

29. (currently amended) The ~~synthetic DNA~~ promoter of claim 20, wherein minimal domain (b) is SEQ ID NO: 5.

Claims 30-38. (canceled).

39. (currently amended) A method for testing the level of expression of a polynucleotide~~gene, in a plant~~ comprising:

~~a) providing a test construct comprising a target gene or reporter gene linked in proper orientation with the synthetic DNA promoter of SEQ ID NO. 1,~~

~~b) providing plant protoplasts,~~

a~~e~~) transforming a ~~the~~ plant protoplast ~~protoplasts~~ with a ~~the~~ test construct, wherein said test construct comprises a polynucleotide encoding a target or reporter polypeptide operably linked with the 3' end of the promoter of claim 20 and wherein said polynucleotide is in frame with SEQ ID NO:16 of said promoter~~using polyethylene glycol (PEG) mediated transformation, and~~

bd) performing a transient GUS assay using the transformed plant protoplast of (a), and

(c) comparing the assay results of (b) ~~to compare the expression of the test construct~~ with results from a transient GUS assay performed using a plant protoplast transformed with a control construct, wherein said control construct comprises said polynucleotide encoding a target or reporter polypeptide of (a) operably linked with ~~that of the same target gene or reporter gene under the control of a natural~~ a CaMV 35S promoter ~~showing the desired level of activity~~, thereby testing the level of expression of a polynucleotide.

40. (currently amended) The method of claim 39, wherein said ~~the~~ plant protoplast is a protoplast selected from the group consisting of a tobacco protoplast , a cotton protoplast, a cabbage protoplast and~~or~~ a potato protoplast.

41. (currently amended) The method of claim 39, wherein the protoplast is ~~protoplasts are~~ derived from a plant tissue.

42. (currently amended) The method of claim 41, wherein the plant tissue is a plant tissue selected from the group consisting of a root, shoot, leaf and ~~or~~ storage tissue.

43. (currently amended) The method of claim 39, wherein the polynucleotide encoding a target or reporter polypeptide ~~gene~~ is *uidA*.

44. (currently amended) The ~~A~~ method of claim 39 wherein said transformation is performed using polyethylene glycol-mediated transformation or biolistic-mediated transformation~~for testing the level of expression of a gene in a plant comprising:~~

~~a) providing a test construct comprising a target gene or reporter gene linked in proper orientation with the synthetic DNA promoter of SEQ ID NO. 1,~~

~~b) providing plant protoplasts,~~

~~b) transforming the plant protoplasts with the test construct using biolistic-mediated transformation, and~~

~~c) performing a transient GUS assay to compare the expression of the test construct with that of the same target gene or reporter gene under the control of a natural CaMV 35S promoter showing the desired level of activity~~.

Claims 45-52. (canceled).